

GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: October 22, 2001, 01:27:29 ; Search time 17.02 Seconds  
(without alignments)  
3306.802 Million cell updates/sec

Title: US-09-515-806-2  
Perfect score: 1643  
Sequence: 1 MAGRGARGRDEPPESYP.....YNIKVKVSVFLYSYRDD 1643

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	0.7	576	1	POLO_DROME
2	10	0.6	298	1	KPFS_HUMAN
3	10	0.6	323	1	KRAF_MSV36
4	10	0.6	328	1	KRAB_MOUSE
5	10	0.6	367	1	RMIL_AVITII
6	10	0.6	380	1	KRAA_MOUSE
7	10	0.6	437	1	KRAA_MOUSE
8	10	0.6	450	1	RMIL_AVEVR
9	10	0.6	547	1	YMXI_CABEL
10	10	0.6	603	1	PLKI_HUMAN
11	10	0.6	603	1	PLKI_MOUSE
12	10	0.6	603	1	PLKI_MOUSE
13	10	0.6	604	1	KRAA_MOUSE
14	10	0.6	606	1	KRAA_MOUSE
15	10	0.6	606	1	KRAA_MOUSE
16	10	0.6	638	1	KRAF_PIG
17	10	0.6	647	1	KRAF_XENLA
18	10	0.6	648	1	KRAF_CHICK
19	10	0.6	648	1	KRAF_HUMAN
20	10	0.6	648	1	KRAF_HUMAN
21	10	0.6	765	1	KRAF_HUMAN
22	10	0.6	781	1	KRAF_MOUSE
23	10	0.6	806	1	KRAF_MOUSE
24	10	0.6	807	1	RMIL_CHICK
25	9	0.5	813	1	KRAF_CABEL
26	9	0.5	294	1	KRAF_MOUSE
27	9	0.5	402	1	KRAF_MOUSE
28	9	0.5	507	1	KRAF_MOUSE
29	9	0.5	515	1	KRAF_MOUSE
30	9	0.5	609	1	KRAF_MOUSE
31	9	0.5	617	1	KRAF_MOUSE
32	9	0.5	620	1	KRAF_MOUSE
33	9	0.5	626	1	KRAF_MOUSE
34	9	0.5	683	1	KRAF_MOUSE

34	9	0.5	764	1	UBF1_HUMAN
35	9	0.5	764	1	UBF1_RAT
36	9	0.5	1062	1	CC7_SCHPO
37	9	0.5	1187	1	TKN2_HUMAN
38	9	0.5	1590	1	GCN2_YEAST
39	9	0.5	2347	1	KROS_HUMAN
40	9	0.5	2554	1	7LES_DROME
41	9	0.5	2594	1	7LES_DROME
42	8	0.5	111	1	HIS2_AZOB
43	8	0.5	166	1	LITE_HUMAN
44	8	0.5	217	1	SODP_LYCES
45	8	0.5	219	1	SODP_PETHY

## ALIGNMENTS

RESULT 1	
POLO_DROME	
ID	POLO_DROME
AC	P52304
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	PROTEIN KINASE POLO (EC 2.7.1.-)
GN	POLO
OS	Drosophila melanogaster (Fruit fly)
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CANTON-S;
RC	MEDLINE=92084090; PubMed=1660828;
RA	Llanazares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
RA	Gonzalez C., Kares R.E., Glover D.M., Sunkel C.E.;
RT	"Polo encodes a protein kinase homolog required for mitosis in
RT	Drosophila";
RL	Genes Dev. 5:2153-2165(1991).
CC	FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC	CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC	TISSUE SPECIFICITY: CYTOPLASMIC.
CC	SUBCELLULAR LOCATION: LARVAL DISCS, BRAIN AND TESTIS.
CC	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	CD5/POLO SUBFAMILY.
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	EMBL: X63361; CAA44963.1; -
DR	HSP; P11362; IFGI.
DR	FlyBase: FBgn0003124; polo.
DR	InterPro: IPR000719; -
DR	InterPro: IPR000959; -
DR	InterPro: IPR002290; -
DR	Pfam: PF00659; polo_box; 2.
DR	Pfam: PF00659; pkinase; 1.
DR	PROSITE: PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR	PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR	PROSITE: PS00111; PROTEIN KINASE DOM; 1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.
FT	DOMAIN 25 277 PROTEIN KINASE
FT	NP_BIND 31 39 ATP (BY SIMILARITY)
FT	BINDING 54 54 ATP (BY SIMILARITY)
FT	ACT_SITE 148 148 BY SIMILARITY
FT	DOMAIN 391 420 POLO-HOMOLOGY (PH2)
SQ	SEQUENCE 576 AA; 66947 MW; B957BDAL73FA57D3 CRC64;

Mon Oct 22 08:29:39 2001

Query Match 0.7%; Score 11; DB 1; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Indels 0; Gaps 0;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 861 HVKIGDFGLAT 871  
 DB 161 HVKIGDFGLAT 171

RESULT 2  
 ID KPKS\_HUMAN STANDARD; PRT; 298 AA.  
 AC P07557;  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE PK PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)  
 DE (ONCOGENE PKS1) (FRAGMENT).  
 GN ARAF2 OR PKS OR PKS1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=86313571; PubMed=3529082;  
 CC Mark G.E., Seeley T.W., Shows T.B., Mountz J.D.;  
 CC "PKs, a raf-related sequence in humans";  
 CC Proc. Natl. Acad. Sci. U.S.A. 83:6312-6316(1986).  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -----  
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 CC -----  
 CC EMBL; M13829; AAB08754.1; -;  
 CC PIR; A23541; TVHUPK.  
 CC HSSP; P00523; 2PTK.  
 CC InterPro; IPR000719; -;  
 CC InterPro; IPR002290; -;  
 CC Pfam; PF00069; pkinase; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Transferrase; Serine/threonine-protein kinase; Proto-oncogene;  
 CC ATP-binding.  
 CC NON\_TER 1 1 PROTEIN KINASE.  
 CC DOMAIN 19 279  
 CC NP\_BIND 25 33 ATP (BY SIMILARITY).  
 CC BINDING 45 45 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 138 138 BY SIMILARITY.  
 CC SEQUENCE 298 AA; 33852 MW; 9AC38F66A7AAFD00 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 0.099;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 DB 152 VKIGDFGLAT 161

RESULT 3  
 ID KRAF\_MSV36 STANDARD; PRT; 323 AA.  
 AC P00532;

DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE RAF SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN (EC 2.7.1.1-).  
 DE V-RAF.  
 GN Murine sarcoma virus 3611.  
 OS Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses.  
 OC NCBI\_TaxID=11812;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=84121298; PubMed=6320371;  
 CC Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;  
 CC "A common onc gene sequence transduced by avian carcinoma virus MH2  
 CC and by murine sarcoma virus 3611";  
 CC Science 223:813-816(1984).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=84172180; PubMed=6324342;  
 CC Mark G.E., Rapp U.R.;  
 CC "Primary structure of v-raf: relatedness to the src family of  
 CC oncogenes";  
 CC Science 224:285-289(1984).  
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-RAF  
 CC POLYPEPTIDE.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; K01691; AAA46579.1; ALT\_INIT.  
 CC PIR; A06638; TVWVF6.  
 CC HSSP; P11362; IFGI.  
 CC InterPro; IPR000719; -;  
 CC InterPro; IPR002290; -;  
 CC Pfam; PF00069; pkinase; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Polyprotein; Transforming protein; Serine/threonine-protein kinase;  
 CC Transferrase; Oncogene; ATP-binding.  
 CC DOMAIN 24 284 PROTEIN KINASE.  
 CC NP\_BIND 30 38 ATP (BY SIMILARITY).  
 CC BINDING 50 50 ATP (BY SIMILARITY).  
 CC ACT\_SITE 143 143 BY SIMILARITY.  
 CC SEQUENCE 323 AA; 36883 MW; 52A5423A66E362F3 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 DB 157 VKIGDFGLAT 166

RESULT 4  
 ID KRAF\_MOUSE STANDARD; PRT; 328 AA.  
 AC P28028;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE B-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)  
 DE (FRAGMENT).  
 GN BRAF OR B-RAF.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91271351; PubMed=2052597;  
 RA Miki T., Fleming T.P., Crescenzi M., Molloy C.J., Blam S.B.,  
 RA Reynolds S.H., Aaronson S.A.;  
 RT "Development of a highly efficient expression cDNA cloning system:  
 RT application to oncogene isolation."  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5167-5171(1991).  
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.  
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF  
 CC HIPPOCAMPAL NEURON.  
 CC -!- DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES  
 CC A TIFIA-BRAF (T18) ONCOGENE ORIGINALLY ISOLATED FROM A FURFURAL-  
 CC INDUCED HEPATOMA.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
 -----  
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 -----  
 DR EMBL; M64429; AAA37320.1; ALT\_INIT.  
 DR PIR; A40951; TVMSBF.  
 DR HSSP; P11362; IFGI.  
 DR MGD; MGI:88190; Braf.  
 DR InterPro; IPR000719; -.  
 DR InterPro; IPR002290; -.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferase; Serine/threonine-protein kinase; Proto-oncogene;  
 KW ATP-binding; Chromosomal translocation.  
 FT NON\_TER 1 1  
 FT DOMAIN 19 279 PROTEIN KINASE.  
 FT NP\_BIND 25 33 ATP (BY SIMILARITY).  
 FT BINDING 45 45 ATP (BY SIMILARITY).  
 FT ACT\_SITE 138 138 BY SIMILARITY.  
 SQ SEQUENCE 328 AA; 36986 MW; 67A2EBFB78A78E3D CRC64;

Query Match 0.6%; Score 10; DB 1; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 862 VKIGDFGLAT 871  
 |||||  
 DB 152 VKIGDFGLAT 161

RESULT 5  
 RMIL\_AVII  
 ID RMIL\_AVII STANDARD; PRT; 367 AA.  
 AC P10533; Q85612; Q85613; Q85614;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE RMIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN  
 DE (EC 2.7.1.-).  
 GN V-RML.  
 OS Avian retrovirus IC10.  
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.  
 OX NCBI\_TaxID=11874;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=89160254; PubMed=2537952;  
 RA Eychene A., Marx M., Dezelic P., Calothy G.;  
 RT "Complete nucleotide sequence of IC10, a retrovirus containing the  
 RT Rml oncogene transduced in chicken neuroretina cells infected with  
 RL avian retrovirus RAV-1";  
 RL Nucleic Acids Res. 17:1250-1250(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89091077; PubMed=2850163;  
 RA Marx M., Eychene A., Laugier D., Bechade C., Crisanti P.,  
 RA Dezelee P., Pessac B., Calothy G.;  
 RT "A novel oncogene related to c-mil is transduced in chicken  
 RT neuroretina cells induced to proliferate by infection with an avian  
 RT lymphomatous virus";  
 RL EMBO J. 7:3369-3373(1988).  
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL  
 CC POLYPEPTIDE.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
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 DR EMBL; X13744; CAA32008.1; ALT\_SEQ.  
 DR EMBL; X13438; CAA31790.1; ALT\_SEQ.  
 DR PIR; S01645; TVFVMI.  
 DR HSSP; P11362; IFGI.  
 DR InterPro; IPR000719; -.  
 DR InterPro; IPR002290; -.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR Polyprotein; Transforming protein; Serine/threonine-protein kinase;  
 KW Transferase; Oncogene; ATP-binding.  
 FT DOMAIN 67 327 PROTEIN KINASE.  
 FT NP\_BIND 73 81 ATP (BY SIMILARITY).  
 FT BINDING 93 93 ATP (BY SIMILARITY).  
 FT ACT\_SITE 186 186 BY SIMILARITY.  
 SQ SEQUENCE 367 AA; 41023 MW; E137AFCDECB9398A CRC64;

Query Match 0.6%; Score 10; DB 1; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 862 VKIGDFGLAT 871  
 |||||  
 DB 200 VKIGDFGLAT 209

RESULT 6  
 KMIL\_AVIMH  
 ID KMIL\_AVIMH STANDARD; PRT; 380 AA.  
 AC P00531;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE MIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN  
 DE (EC 2.7.1.-).  
 GN V-MIL OR V-MHT.  
 OS Avian retrovirus MH2.  
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.  
 OX NCBI\_TaxID=11870;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84191511; PubMed=6325930;  
 RA Suttrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,

Bister K.;  
 "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine retroviral oncogene v-raf";  
 Nature 309:85-88(1984).  
 [2]  
 SEQUENCE FROM N.A.  
 MEDLINE=84121298; PubMed=6320371;  
 Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;  
 "A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611";  
 Nature 223:813-816(1984).  
 CC -1- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING CAPACITY BUT IT ABOLISHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN MACROPHAGES TRANSFORMED BY OTHER ONCOGENES.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-MHT OR GAG-MIL POLYPROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
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 CC  
 CC EMBL; X00534; CAA25211.1; ALT\_INIT.  
 CC PIR; A00639; TVFVMM.  
 CC HSP; P11362; IFGI.  
 CC InterPro; IPR000719; .  
 CC InterPro; IPR002290; .  
 CC Pfam; PF00069; pkinase; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Polyprotein; Transforming protein; Serine/threonine-protein kinase;  
 KW Transferase; Oncogene; ATP-binding.  
 FT DOMAIN 82 341 PROTEIN KINASE.  
 FT NP\_BIND 88 96 ATP (BY SIMILARITY).  
 FT BINDING 108 108 ATP (BY SIMILARITY).  
 FT ACT\_SITE 201 201 BY SIMILARITY.  
 FT CONFLICT 211 211 G -> E (IN REF. 2).  
 FT SEQUENCE 380 AA; 42853 MW; 6498695FB7EBE5D CRC64;  
 SQ  
 Query Match 0.6%; Score 10; DB 1; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 862 VKIGDFGLAT 871  
 DB 215 VKIGDFGLAT 224  
 RESULT 7  
 KRAA\_MOUSE  
 ID KRAA\_MOUSE STANDARD; PRT; 437 AA.  
 AC P04627;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (FRAGMENT).  
 DE ARAF1 OR ARAF OR A-RAF.  
 GN Mus musculus (Mouse)  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87064566; PubMed=3491291;  
 RA Hufelhel M., Goldsborough M., Cleveland J., Gunnell M., Bonner T.,

Rapp U.R.;  
 "Characterization of murine A-raf, a new oncogene related to the v-raf oncogene";  
 Mol. Cell. Biol. 6:2655-2662(1986).  
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
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 CC  
 CC EMBL; D00024; BAA00019.1; .  
 CC EMBL; M13071; AAA37258.1; .  
 CC PIR; A25382; TVMSRF.  
 CC HSP; P11362; IFGI.  
 CC MGD; MGI:88065; Araf.  
 CC InterPro; IPR000719; .  
 CC InterPro; IPR002290; .  
 CC Pfam; PF00069; pkinase; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Transferase; Serine/threonine-protein kinase; Proto-oncogene;  
 KW ATP-binding.  
 FT DOMAIN 141 401 PROTEIN KINASE.  
 FT NP\_BIND 147 155 ATP (BY SIMILARITY).  
 FT BINDING 167 167 ATP (BY SIMILARITY).  
 FT ACT\_SITE 260 260 BY SIMILARITY.  
 FT SEQUENCE 437 AA; 48702 MW; 1534011B018710ED CRC64;  
 SQ  
 Query Match 0.6%; Score 10; DB 1; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 862 VKIGDFGLAT 871  
 DB 274 VKIGDFGLAT 283  
 RESULT 8  
 RMIL\_AVEVR  
 ID RMIL\_AVEVR STANDARD; PRT; 450 AA.  
 AC P27966;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE RMIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN (EC 2.7.1.-).  
 GN V-RML.  
 OS Avian rous-associated virus type 1.  
 OC Viruses; Retroviridae; Retroviridae; Avian type C retroviruses.  
 OC NCBI\_TaxID=11950;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91251215; PubMed=1645786;  
 RA Felger M.P., Eychene A., Barnier J.V., Calogeraki I., Calothy G., Marx M.;  
 RT "Common mechanism of retrovirus activation and transduction of c-mil and c-Rml in chicken neuroretina cells infected with Rous-associated virus type 1";  
 RL J. Virol. 65:3633-3640(1991).  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL-ENV POLYPROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.

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 CC -----

DR EMBL; M62407; AAA42549.1; -  
 DR PIR; A40341; TVFVNR.  
 DR HSP; P11362; IFGI.  
 DR InterPro; IPR000719; -  
 DR InterPro; IPR002290; -  
 DR Pfam; PF00069; pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR Polyprotein; Transforming protein; Serine/threonine-protein kinase;  
 KW Transferase; Oncogene; ATP-binding.  
 FT DOMAIN 83 343 PROTEIN KINASE.  
 FT NP\_BIND 89 97 ATP (BY SIMILARITY).  
 FT BINDING 109 109 ATP (BY SIMILARITY).  
 FT ACT\_SITE 202 202 BY SIMILARITY.  
 SQ SEQUENCE 450 AA; 50313 MW; 6581AAF2253CB622 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0;

QY 862 VKIGDFGLAT 871  
 |||||  
 DB 216 VKIGDFGLAT 225

RESULT 9  
 ID YMX1\_CAEEL STANDARD; PRT; 547 AA.  
 AC P34509.  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE PUTATIVE SERINE/THREONINE-PROTEIN KINASE K06H7.1 IN CHROMOSOME III  
 DE (EC 2.7.1.1).  
 GN K06H7.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 RA Wohldman P.;  
 RT \*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.\*  
 RL Nature 368:32-38(1994).  
 CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-  
 CC PROTEIN KINASES.  
 CC -----

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DR EMBL; L15314; AAA28084.1; -  
 DR PIR; S4841; S4841.  
 DR HSP; Q63450; IA06.  
 DR Wormpep; K06H7.1; CE00252.  
 DR InterPro; IPR000719; -  
 DR InterPro; IPR002290; -  
 DR Pfam; PF00069; pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;  
 KW ATP-binding.  
 FT DOMAIN 267 526 PROTEIN KINASE.  
 FT NP\_BIND 273 281 ATP (BY SIMILARITY).  
 FT BINDING 296 296 ATP (BY SIMILARITY).  
 FT ACT\_SITE 390 390 BY SIMILARITY.  
 SQ SEQUENCE 547 AA; 63490 MW; 0CD28C2FEAC63101 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 547;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0;

QY 862 VKIGDFGLAT 871  
 |||||  
 DB 404 VKIGDFGLAT 413

RESULT 10  
 ID PLK1\_HUMAN

PLK1\_HUMAN STANDARD; PRT; 603 AA.  
 AC P53350;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.1) (PLK-1) (SERINE-  
 DE THREONINE PROTEIN KINASE 13) (StpK13).  
 GN PLK OR PLK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=94289293; PubMed=8018557;  
 RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,  
 RA Ferris D.K.;  
 RT "Cloning and characterization of human and murine homologues of the  
 RT Drosophila polo serine-threonine kinase."  
 RL Cell Growth Differ. 5:249-257(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94067140; PubMed=7902533;  
 RA Lake R.J., Jellinek W.R.;  
 RA "Cell cycle- and terminal differentiation-associated regulation of  
 RT the mouse mRNA encoding a conserved mitotic protein kinase."  
 RT Mol. Cell. Biol. 13:7793-7801(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95051109; PubMed=7962193;  
 RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,  
 RA Nigg E.A.;  
 RT "Cell cycle analysis and chromosomal localization of human Plk1, a  
 RT putative homologue of the mitotic kinases Drosophila polo and  
 RT Saccharomyces cerevisiae Cdc5."  
 RL J. Cell Sci. 107:1509-1517(1994).

[4]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=94173904; PubMed=8127874;  
 RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,  
 RA Ruebsamen-Waigmann H., Strehhardt K.;  
 RT "Induction and down-regulation of PLK, a human serine/threonine  
 RT kinase expressed in proliferating cells and tumors.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).  
 CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE  
 CC DURING G1 OR S PHASE.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -!- TISSUE SPECIFICITY: PLACENTA AND COLON.  
 CC -!- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M  
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS  
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN  
 CC DURING S PHASE.  
 CC -!- INDUCTION: BY GROWTH-STIMULATING AGENTS.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CDC5/POLO SUBFAMILY.  
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 CC -----  
 DR EMBL; U01038; AAA56634.1; -;  
 DR EMBL; L19559; AAA36659.1; -;  
 DR EMBL; X73458; CAA51837.1; -;  
 DR EMBL; X75932; CAA53536.1; -;  
 DR HSSP; P11362; 1FGI.  
 DR MM; 602098; -;  
 DR InterPro; IPR000719; -;  
 DR InterPro; IPR000959; -;  
 DR InterPro; IPR002280; -;  
 DR Pfam; PF00659; POLO\_box; 2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW Nuclear protein.  
 KW DOMAIN 53 305 PROTEIN KINASE.  
 FT NP\_BIND 59 67 ATP (BY SIMILARITY).  
 FT BINDING 82 82 ATP (BY SIMILARITY).  
 FT ACT\_SITE 176 176 BY SIMILARITY.  
 FT DOMAIN 410 439 POLO-HOMOLOGY (PH2).  
 FT CONFLICT 2 2 S -> T (IN REF. 1).  
 FT CONFLICT 11 11 A -> P (IN REF. 1).  
 FT CONFLICT 58 58 F -> L (IN REF. 1).  
 FT CONFLICT 60 60 G -> S (IN REF. 1).  
 FT CONFLICT 73 73 A -> V (IN REF. 2).  
 FT CONFLICT 141 141 L -> P (IN REF. 4).  
 FT CONFLICT 227 227 G -> E (IN REF. 4).  
 FT CONFLICT 301 301 N -> G (IN REF. 2).  
 FT CONFLICT 495 495 A -> G (IN REF. 2).  
 FT CONFLICT 501 501 E -> Q (IN REF. 2).  
 SQ SEQUENCE 603 AA; 68254 MW; 178C2F13C10E8206 CRC64;  
 Query Match 0.6%; Score 10; DB 1; Length 603;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 862 VKIGDFGLAT 871  
 Db 190 VKIGDFGLAT 199  
 RESULT 11

PLK1\_MOUSE  
 ID PLK1\_MOUSE STANDARD; PRT; 603 AA.  
 AC Q07832;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (SERINE-  
 DE THREONINE PROTEIN KINASE 13) (STPK13).  
 OS PLK.  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Bone marrow;  
 RX MEDLINE=93281660; PubMed=8099445;  
 RA Clay F.J., McEwen S.J., Bertoncello I., Wilks A.F., Dunn A.R.;  
 RT "Identification and cloning of a protein kinase-encoding mouse gene,  
 RT PLK, related to the polo gene of Drosophila.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=94289293; PubMed=8018557;  
 RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,  
 RA Ferris D.K.;  
 RT "Cloning and characterization of human and murine homologues of the  
 RT Drosophila polo serine-threonine kinase.";  
 RL Cell Growth Differ. 5:249-257(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=94067140; PubMed=7902533;  
 RA Lake R.J., Jelinek W.R.;  
 RT "Cell cycle- and terminal differentiation-associated regulation of  
 RT the mouse mrna encoding a conserved mitotic protein kinase.";  
 RL Mol. Cell. Biol. 13:7793-7801(1993).  
 CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE  
 CC DURING G1 OR S PHASE.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -!- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN  
 CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS.  
 CC OVARY AND TESTES.  
 CC -!- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL  
 CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE  
 CC ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN  
 CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN  
 CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M  
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS  
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN  
 CC DURING S PHASE.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CDC5/POLO SUBFAMILY.  
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 CC -----  
 DR EMBL; L06144; AAA39948.1; -;  
 DR EMBL; U01063; AAA56635.1; -;  
 DR EMBL; L19558; AAA16071.1; -;  
 DR HSSP; P11362; 1FGI.  
 DR MGD; MGI:97621; PLK.  
 DR InterPro; IPR000719; -;  
 DR InterPro; IPR000959; -;  
 DR InterPro; IPR002290; -;  
 DR Pfam; PF00659; POLO\_box; 2.  
 DR Pfam; PF00069; pkinase; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Nuclear protein.  
FT DOMAIN 53 305 PROTEIN\_KINASE.  
FT NP\_BIND 59 67 ATP (BY SIMILARITY).  
FT BINDING 82 82 ATP (BY SIMILARITY).  
FT ACT\_SITE 176 176 BY SIMILARITY.  
FT DOMAIN 410 439 POLO-HOMOLOGY (PH2).  
FT CONFLICT 4 4  
FT CONFLICT 15 15 A -> V (IN REF. 1).  
FT CONFLICT 23 23 A -> T (IN REF. 1).  
FT CONFLICT 27 27 P -> L (IN REF. 1).  
FT CONFLICT 29 29 V -> A (IN REF. 1).  
FT CONFLICT 29 29 G -> S (IN REF. 1).  
FT CONFLICT 41 41 P -> L (IN REF. 1).  
FT CONFLICT 54 54 V -> I (IN REF. 1).  
FT CONFLICT 495 495 A -> R (IN REF. 1).  
SQ SEQUENCE 603 AA; 68300 MW; 1B980646366EFA10 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 603;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871

Db 190 VKIGDFGLAT 199

## RESULT 12

PLK1\_RAT STANDARD; PRT; 603 AA.  
AC Q62673;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1).  
GN PLK  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RA Amstrup J., Hansen J.A., Hxirlis Nielsen J.;  
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE  
CC DURING G1 OR S PHASE (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC CDC5/POLO SUBFAMILY.

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DR EMBL; U10188; AA18885.1; -  
DR HSSP; P47811; IP38.  
DR InterPro; IPR000719; -  
DR InterPro; IPR000959; -  
DR InterPro; IPR002290; -  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00659; POLO\_box; 2.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;

KW Nuclear protein.  
FT DOMAIN 53 305 PROTEIN\_KINASE.  
FT NP\_BIND 59 67 ATP (BY SIMILARITY).  
FT BINDING 82 82 ATP (BY SIMILARITY).  
FT ACT\_SITE 176 176 BY SIMILARITY.  
FT DOMAIN 410 439 POLO-HOMOLOGY (PH2).  
SQ SEQUENCE 603 AA; 68313 MW; 107AFFB3B7EDC002 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 603;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871

Db 190 VKIGDFGLAT 199

## RESULT 13

KRAA\_RAT STANDARD; PRT; 604 AA.  
AC P14056;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-).  
GN ARAF1 OR A-RAF.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FI-SCHER; TISSUE=Liver;  
RX MEDLINE=88217324; PubMed=3449797;  
RA Ishikawa F., Takaku F., Nagao M., Sugimura T.;  
RT "The complete primary structure of the rat A-raf cDNA coding region:  
RT conservation of the putative regulatory regions present in rat  
RT c-ras";  
RL Oncogene Res. 1:243-253(1987).  
CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
CC FROM THE CELL MEMBRANE TO THE NUCLEUS.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC MIL/RAF SUBFAMILY.  
CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
CC BINDING DOMAIN.

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DR EMBL; X05942; CAA30023.1; -  
DR PIR; S00726; S00726.  
DR HSSP; P04049; IFAQ.  
DR InterPro; IPR000719; -  
DR InterPro; IPR002219; -  
DR InterPro; IPR002290; -  
DR Pfam; PF00130; DAG\_PE\_bind; 1.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00008; DAGPEDOMAIN.  
DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
DR PROSITE; PS00081; DAG\_PE\_BIND\_DOM\_2; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;  
KW ATP-binding; Phorbol-ester binding.  
FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.  
FT DOMAIN 308 568 PROTEIN\_KINASE.



FT NP\_BIND 314 322 ATP (BY SIMILARITY).  
 FT BINDING 334 334 ATP (BY SIMILARITY).  
 FT ACT\_SITE 427 427 BY SIMILARITY.  
 SQ SEQUENCE 604 AA; 67551 MW; FF24FB2170B0B115 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 604;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
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 Db 441 VKIGDFGLAT 450

RESULT 14  
 KRAA\_HUMAN STANDARD; PRT; 606 AA.  
 AC P10396;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)  
 DE (ONCOGENE PKS2).  
 GN ARAF1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87146380; PubMed=30296685;  
 RA Beck T.W., Huleihel M., Gunnell M., Bonner T.I., Rapp U.R.;  
 RT "The complete coding sequence of the human A-raf-1 oncogene and  
 transforming activity of a human A-raf carrying retrovirus.";  
 RL Nucleic Acids Res. 15:595-609(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Placenta;  
 MEDLINE=94292185; PubMed=8020955;  
 RA Lee J.E., Beck T.W., Brennscheidt U., Degennaro L.J., Rapp U.R.;  
 RT "The complete sequence and promoter activity of the human A-raf-1  
 gene (ARAF1).";  
 RL Genomics 20:43-55(1994).

CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
 FROM THE CELL MEMBRANE TO THE NUCLEUS.  
 CC -!- TISSUE SPECIFICITY: PREDOMINANTLY IN UROGENITAL TISSUES (BY  
 SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 BINDING DOMAIN.  
 CC  
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 CC  
 CC EMBL; X04790; CAA38476.1; -;  
 CC EMBL; L24038; AAA65219.1; -;  
 CC EMBL; U01337; AAB03517.1; -;  
 CC PIR; A26439; TVHUAF.  
 CC HSP; P04049; 1FAO.  
 CC MIM; 311010; -;  
 CC InterPro; IPR000719; -;  
 CC InterPro; IPR002219; -;  
 CC InterPro; IPR002290; -;  
 CC Pfam; PF00130; DAG\_PE-bind; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00008; DAGPEDOMAIN.  
 CC

DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;  
 KW ATP-binding; Phorbol-ester binding.  
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.  
 FT NP\_BIND 316 324 ATP (BY SIMILARITY).  
 FT BINDING 336 336 ATP (BY SIMILARITY).  
 FT ACT\_SITE 429 429 BY SIMILARITY.  
 SQ SEQUENCE 606 AA; 67585 MW; D23E5711304AA468 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 606;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871  
 |||||  
 Db 443 VKIGDFGLAT 452

RESULT 15  
 KRAA\_PIG STANDARD; PRT; 606 AA.  
 AC O19004;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.1-)  
 DE (A-RAF-1).  
 GN ARAF1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LANDRACE; TISSUE=Liver;  
 RX MEDLINE=97343844; PubMed=9166601;  
 RA Yasue H., Adams L., Ozawa A., Hanazono M., Li N., Lin Z.H.,  
 RA Kusumoto H.;  
 RT "Assignment of ARAF1 to porcine chromosome Xp11.2-p13 by fluorescence  
 in situ hybridization";  
 RL Mamm. Genome 8:457-458(1997).  
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
 FROM THE CELL MEMBRANE TO THE NUCLEUS (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG  
 BINDING DOMAIN.  
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 CC  
 CC EMBL; D88385; BAA22379.1; -;  
 CC HSP; P04049; 1FAO.  
 CC InterPro; IPR000719; -;  
 CC InterPro; IPR002219; -;  
 CC InterPro; IPR002290; -;  
 CC Pfam; PF00130; DAG\_PE-bind; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00008; DAGPEDOMAIN.  
 CC PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 CC PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.



DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;  
 KW ATP-binding; Phorbol-ester binding.  
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.  
 FT DOMAIN 310 570 PROTEIN KINASE.  
 FT NP\_BIND 316 324 ATP (BY SIMILARITY).  
 FT BINDING 336 336 ATP (BY SIMILARITY).  
 FT ACT\_SITE 429 429 BY SIMILARITY.  
 SQ SEQUENCE 606 AA; 67538 MW; 1A7EEB9A5D9DE152 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 606;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 862 VKIGDFGLAT 871  
 |||||  
 Db 443 VKIGDFGLAT 452

Search completed: October 22, 2001, 01:31:53  
 Job time: 264 sec

